

OM nucleic - nucleic search, using sw model

```
Run on:      June 29, 2002, 22:09:22 ; Search time 17398.4 seconds
              (without alignments)
              3393.169 Million cell updates/sec
```

Title: US-09-303-518D-649
Perfect score: 4374
Sequence: 1 atgaacaacgcgacaacg.....attagctaccgctgtaa 4374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

```
Searched:      13736207 segs, 6748477542 residues
Total number of hits satisfying chosen parameters:    27472414
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 100 summaries
```

Database :

```

1:  em_estha: *
2:  em_esthum: *
3:  em_estlun: *
4:  em_estlun: *
5:  em_estlun: *
6:  em_estlun: *
7:  em_estlun: *
8:  em_estlun: *
9:  em_estlun: *
10:  em_estlun: *
11:  em_estlun: *
12:  em_estlun: *
13:  em_estlun: *
14:  em_estlun: *
15:  em_estlun: *
16:  em_estlun: *

```

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

[illegible]

C	18	46.8	1.1	932	12	CNS00720	AL065742	Drosophila
C	19	46.6	1.1	815	12	CNS0200C	AL175843	Tetrahodon
C	20	46.4	1.1	894	12	CNS01591	AL105168	Drosophila
C	21	46	1.1	696	10	BG717141	BG717141	6027204141
C	22	46	1.1	1101	12	CNS0117YH	AL108659	Drosophila
C	23	45.8	1.0	503	12	BH227007	BH227007	1006136EE
C	24	45.6	1.0	429	9	AW827177	AW827177	UG1_267_ID
C	25	45.6	1.0	658	10	BI955152	BI955152	HVSMEn001
C	26	45.6	1.0	1099	12	CNS03YCU	AL266151	Tetrahodon
C	27	45.4	1.0	504	10	C26583	C26583	C26583
C	28	45.4	1.0	936	12	AG131119	AG131119	Pan trogl
C	29	45.4	1.0	1038	12	CNS02YBW	AL106041	Drosophila
C	30	45.4	1.0	1159	12	CNS015XR	BI2052	IP1020-Sp6
C	31	45.4	1.0	1211	12	BI2052	BI945506	HVSMEL000
C	32	45.2	1.0	937	12	BI945506	AL106054	Drosophila
C	33	45.2	1.0	1203	12	AC060162	AG060162	Pan trogl
C	34	45	1.0	1203	12	AC060162	AL106750	Drosophila
C	35	45	1.0	1101	12	CNS016HG	AL163586	AU163586
C	36	44.8	1.0	440	9	AU163586	AL1076850	Drosophila
C	37	44.8	1.0	977	12	CNS00JX7	AL1076850	Drosophila
C	38	44.8	1.0	1101	12	CNS0170B	AL108229	Drosophila
C	39	44.6	1.0	813	10	BG727321	BG727321	602722423
C	40	44.6	1.0	1033	10	BG415913	BG415913	HVSMEL000
C	41	44.4	1.0	415	12	BH630431	BH630431	1007088D1
C	42	44.4	1.0	551	12	BI140958	BI140958	IP1_41.DO
C	43	44.4	1.0	570	10	BI076151	BI076151	IP1_26.B1
C	44	44.4	1.0	826	10	BF626822	BF626822	HVSMEn000
C	45	44.4	1.0	946	9	AI069309	AI069309	msae0006
C	46	44.2	1.0	1101	12	CNS00BNG	AL057338	Drosophila
C	47	44	1.0	937	12	CNS006ST	AL065880	Drosophila
C	48	43.8	1.0	487	10	BE917810	BE917810	OVI_7.D07
C	49	43.8	1.0	520	10	BE917892	BE917892	OVI_7.D07
C	50	43.8	1.0	844	12	CNS0052P	AL056652	Drosophila
C	51	43.8	1.0	1296	12	BG768629	BG768629	SEAMC006
C	52	43.6	1.0	355	9	AA798861	AA798861	v994810.r
C	53	43.4	1.0	917	12	CNS00CUT	AL059857	Drosophila
C	54	43.4	1.0	1129	12	CNS00LOS	AL0676824	Drosophila
C	55	43.2	1.0	412	9	AMS63687	AMS63687	LG1_245_A
C	56	43.2	1.0	675	9	AL507356	AL507356	AL507356
C	57	43	1.0	315	12	CNS01677	AL106381	Drosophila
C	58	43	1.0	703	10	BF628603	BF628603	HVSMEn000
C	59	43	1.0	890	12	CNS035KB	AL1228836	Tetrahodon
C	60	43	1.0	955	12	CNS00ESP	AL069794	Drosophila
C	61	43	1.0	1071	12	CNS00EWT	AL069395	Drosophila
C	62	42.8	1.0	375	10	BG437344	BG437344	EM1_51.D1
C	63	42.8	1.0	399	10	BG464276	BG464276	EM1_71.G0
C	64	42.8	1.0	399	10	BI246104	BI246104	IP1_68.H0
C	65	42.8	1.0	436	10	BG556829	BG556829	EM1_39.B0
C	66	42.8	1.0	494	10	BG047881	BG047881	OVI_28.H0
C	67	42.8	1.0	512	9	AW924434	AW924434	WS1_69_A0
C	68	42.8	1.0	519	10	BG355430	BG355430	EM1_16.D0
C	69	42.8	1.0	577	10	BG947889	BG947889	IP1_6.E10
C	70	42.8	1.0	578	10	BG947859	BG947859	IP1_6.B10
C	71	42.8	1.0	584	9	AL500293	AL500293	AL500293
C	72	42.8	1.0	598	10	BI076172	BI076172	IP1_26.E1
C	73	42.8	1.0	953	12	CNS017Y4	AL108132	Drosophila
C	74	42.8	1.0	1101	12	CNS017YU	AG082212	Pan trogl
C	75	42.6	1.0	906	12	AC082212	AU089598	AU089598
C	76	42.4	1.0	363	9	AU089598	AL0640753	AV640753
C	77	42.4	1.0	382	9	AV640753	AV835255	AV835255
C	78	42.4	1.0	626	9	AV835255	AL1000359	Drosophila
C	79	42.4	1.0	852	12	CNS011JX	BI351528	IP1_72_A0
C	80	42.2	1.0	291	10	BI351528	AV202839	AV202839
C	81	42.2	1.0	360	9	AV202839	AV926600	AV926600
C	82	42.2	1.0	504	9	AV926600	AW962555	HVSMEn000
C	83	42.2	1.0	560	9	AW962555	BI958285	BI958285
C	84	42.2	1.0	654	10	BI958285	BI959392	HVSMEn001
C	85	42.2	1.0	657	9	AL504705	AL504705	AL504705
C	86	42.2	1.0	676	9	AL504705	BF631694	HVSMEn001
C	87	42.2	1.0	807	10	BF631694	BF253829	HVSMEn000
C	88	42.2	1.0	868	10	BF253829	BI952167	HVSMEn000
C	89	42.2	1.0	877	10	BI952167	BI958121	HVSMEn001
C	90	42.2	1.0	888	10	BI958121		

see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wang R, Kleinof A, Wise R (2001) Genetically and physically anchored EST resources for

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source
1. .910
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_1lb="RPC1-98"
/clone="BACRI4J21"
/note="end : T77"

BASE COUNT      202 a      63 c      112 g      198 t      335 others
ORIGIN

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[illegible]

Db	580	CSCCMASCCCCGCVSGCSCCSGMSGCCCGCCAGACATCACCHMSAGCMG	533
RESULT	19		
CNS0200C			
LOCUS			
DEFINITION	CNS0200C	815 bp	DNA linear GSS 12-MAY-2000
VERSION	Tetradon nigroviridis genome survey sequence T7 end of clone		
KEYWORDS	222108 of library G from Tetradon nigroviridis, genomic survey		
SOURCE	sequence.		
ORGANISM	ALI75845.1	GI:7813902	
	GSS; genome survey sequence.		
	Tetradon nigroviridis.		
	Tetradon nigroviridis		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
	Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;		
	Tetraodonidae; Tetraodon.		
	1 (bases 1 to 815)		
	Rouneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and		
	Weissenbach,J.		
	Characterization and repeat analysis of the compact genome of the		
	Freshwater pufferfish Tetraodon nigroviridis		
	Unpublished		
	2 (bases 1 to 815)		
	Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,		
	Bernot,A., Fizames,C., Wincker,P., Brottier,P., Queller,F.,		
	Saurin,W. and Weissenbach,J.		
	Human gene number estimate provided by genome wide analysis using		
	Tetradon nigroviridis DNA sequence		
	Unpublished		
	3 (bases 1 to 815)		
	Genoscope.		
	Direct Submission		
	Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases		
	This sequence is a single read and was generated as part of a large		
	scale clone-end sequencing project of the Tetradon nigroviridis		
	genome. For more information, please take a look at		
	http://www.genoscope.cns.fr/Tetraodon.		
	Location/Qualifiers		
	1..815		
	/organism="Tetradon nigroviridis"		
	/db_xref="taxon:99883"		
	/clone="222108"		
	/clone_1lb="G"		
	/note="Genoscope sequence ID : C0AG222DF04LP1-end : T7"		
BASE COUNT	324 a	105 c	281 g 86 t 19 others
ORIGIN			
Query Match	1.1%; Score 46.6; DB 12; Length 815;		
Best Local Similarity	47.4%; Pred. No.2.6;		
Matches 118; Conservative	6; Mismatches 125; Indels 0; Gaps 0;		
QY	3171	ggtcaagaagaaagatgccttcgcacaactcggcaaggcgagacgaacaaaacsagcgga	3230
Db	496	GGACAAGAAGAGAGAGAGAGCAAGGAAGAGAGAGAGAGACAAAGAGAGAGA	555
QY	3331	aaaaagaacgcggaagcccttgacgcgtattcgccggccgagcgcatgccgcgcgaaa	3290
Db	556	GAAAGCAAGAAGAACAGAGAGAGGACACAAAGAAAGAGAGGCGAGACAAAGAGAGA	615
QY	3291	gacagaagcgttgcgaaccgcgcgcgacgagcgagcgcggggaaaaagtgcgcatatgca	3350
Db	616	GGAGCAGACGAAGAAGAGAGAGGCGGAGGMAAAGAAAAGAGAGAGACARGAARA	675
QY	3351	ggcgaagagagaaaaaacgggtgcgagcgagataaagacacgccttgcggaacgcg	3410
Db	676	ARRGGGCGGARACARAAAAARAGAGAGAGACAAAGAAAAMAAARGGARACAAAGA	735
QY	3411	cgaagcgca 3419	

COMMENT

Determination of this BAC and sequence was carried out as part of a collaboration with the European Drosophila Genome Project (<http://www.edgp.ebi.ac.uk>). This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Balland at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

Query Match	1.1%;	Score 46;	DB 12;	Length 1101;
Best Local Similarity	30.1%;	Pred. No. 4.3;		
Matches 101;	Conservative 75;	Mismatches 160;	Indels 0;	Gaps 0

[illegible]

RESULT	23
BH227007/C	
LOCUS	BH227007
DEFINITION	1006136E03.y1 1006 - Rescuedu Grid G Zea mays genomic, DNA sequence.

email: Walidp@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1006136 row: 30
Class: transposon-tagged.

FEATURES	BASE COUNT	ORIGIN
Location/Qualifiers	63 a	190 c 165 g 84 t 1 others
1..503		
/organism="Zea mays"		
/cultivar="mixed background W23/A186/B73"		
/db_xref="taxon:4577"		
/clone_11b="1006 - RescueMu Grid G"		
/issue_type="leaf"		
/dev_stage="adult"		
/lab_host="DH10B"		
/note="Organ: leaf; Vector: RescueMu (engineered from plasmidScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."		

[illegible]

RESULT 24	LOCUS	DEFINITION
AM287177/c	429 bp	linear EST 19-JUL-2000
AM287177	Light Grown 1 (LGI)	Sorghum bicolor cDNA, mRNA
LGI_267_d12.b1_A002		

ACCESSION	SEQUENCE
VERSION	AM287177
KEYWORDS	AM287177.2 GI:6859103
SOURCE	EST.
ORGANISM	Sorghum.
REFERENCE	Sorghum bicolor
AUTHORS	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
JOURNAL	clade; Panicoideae; Andropogoneae; Sorghum.
COMMENT	1 (bases 1 to 429) Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H. An EST database from Sorghum: Light-grown seedlings Unpublished (2000) On Jan 6, 2000 this sequence version replaced gi:6677021. Contact: Cordonnier-Pratt MM Department of Botany The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 542 1805 Email: mmpratt@uga.edu Sequences have been trimmed to exclude polyA, vector and regions below phred quality 16. The threshold for highest quality sequence is 20. Seq primer: JEN REV High quality sequence stop: 332 POLYA-No.
FEATURES	
source	location/Qualifiers 1..429 /organism="Sorghum bicolor" /db_xref="taxon:4558" /clone_lib="Light Grown 1 (Lg1)" /note="Organ: 10- to 14-day-old light-grown (greenhouse) seedlings; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI ; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."
BASE COUNT	51 a 190 c 135 g 53 t
ORIGIN	
Query Match	1.0%; Score 45.6; DB 9; Length 429;
Best Local Similarity	52.7%; Pred. No. 3.4;
Matches	99; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY	3765 gcaacaacgagacgaaacacacttcgaagcagcgcatcggaactcggcagcgcttgcca 3824
DB	3178 GCAGGCCCTCATCGAAGCCACGTCGACACGCGCCGCTACCTGGCACGCGCTTGCCGA 319
QY	3825 cggcgccgcttttcgggcaatacgcacatcgacaggtttctacatcgcgatcagcgcgcgcc 3884
DB	318 TGGCCCCCGCGCGGCGGAACTCGTCGCTGATCTTCCGCCGCCCGGCTTCCCGGAGCGCG 259
QY	3885 ggggttttaagcagcgagacgttcacagcgcgatcggaaggcaaatccgcgcgcgctgct 3944
DB	258 GCGCCGACGCGGCGGCGCGCTCGGCGCGGCGAGAGAGCGTAAAGCGCGCGCGCGGT 199
QY	3945 gcaatcgc 3952
DB	198 TGAAGAGG 191
RESULT	25
LOCUS	B1958152 658 bp mRNA linear EST 22-OCT-2001
DEFINITION	HVSMNH0013K09f Hordeum vulgare rachis EST library HVCNMA015
ACCESSION	(normal) Hordeum vulgare cDNA clone HVSMNH0013K09f, mRNA sequence.
VERSION	B1958152
KEYWORDS	B1958152.1 GI:16309407
SOURCE	EST.
ORGANISM	barley. Hordeum vulgare Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Hordeum. 1 (bases 1 to 658)
AUTHORS	Wing,R., Close,T.J., Kleinofs,A., Wise,R., Chin,A., Begum,D, Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons .J., Oates,R. and Main,D. Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library Unpublished (2001)
TITLE	Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel.: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Total hg bases=276 Seq primer: AATTACCCCTCACTAAAGGG High quality sequence start: 2 High quality sequence stop: 573.
JOURNAL	Location/Qualifiers
COMMENT	1..658 /organism="Hordeum vulgare" /cultivar="Morex" /db_xref="taxon:4513" /clone="HWSMEM0013K09f" /clone_lib="Hordeum vulgare rachis EST library HVCMD0015 (normal)" /tissue="Rachis" /lab_host="TJUC121" /note-Vector: pluescript SK(-); Site.1: EcoRI; Site.2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinofs lab). In the TJ Close lab at the university of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley . To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/g9pages/bgrn/31/clover.html)"
BASE COUNT	93 a 211 c 239 g 106 t 9 others
ORIGIN	
Query Match	1.0%; Score 45.6; DB 10; Length 658;
Best Local Similarity	51.6%; Pred.No.4.2; Mismatches 93; Indels 0; Gaps 0;
Matches	99; Conservative
OY 3786	cctcgcagcagcatcggaactcggcaaggcttcgccacggccgcgtttcgggcaata 3845
DB 357	
	CNCGGCGGGCGGGCGGTACGAGGCANCGTCGTGAGGCGGAGGGCGGCTACACNG 416
OY 3846	cggcatcgacaagttctaactcggatcagcgcgcgggcgcggttttaagcagcgagacct 3905
DB 417	
	AGCGCGGCGGGCGGTTCATCGAGGTGCGGCANCGGCGGGCGGGCGGCTACGCGCACGCC 476
OY 3906	ttcagagcgcatcggagggcaaatccgcgcgcgcgctgtcgtcattacggcattcaaggcacg 3965
DB 477	
	TGACGGCGGGCGGCGCTACCGCGGCTCGGGCGGCGCTACGCGTGCGACGCCGGGCGG 536

[illegible]

OY	3853	gaagatctcaactccgacatcgacgcggcggttttagcaggcgacctttaaagc	3912
Db	614	AACAGCACTACGGCAGCACRACAAACCAGAGACAACAGCTGTCCGACATCTCGTCGCAC	673
OY	3913	ggcatctggaggccaataatccgccgcgcg	3938
Db	674	AACAGCTGCAGCAACTACAAACAGCCG	699

RESULT 27
C26583/c
LOCUS C26583 504 bp mRNA linear EST 06-AUG-1997
DEFINITION C26583 Rice callus cDNA Oryza sativa CDNA clone C12645_1A, mRNA sequence.
ACCESSION C26583
VERSION C26583.1 GI:2310428
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzeae; Oryza.
1 (bases 1 to 504)
Yamamoto, K. and Sasaki, T.
Rice cDNA from callus 1997
Unpublished (1997)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel.: 81-298-38-7441
Fax: 81-298-38-7468
Email: tssasaki@nri.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.

FEATURES	
Source location/Qualifiers	
1..504	
/organism="Oryza sativa"	
/cultivar="Nipponbare"	
/db_xref="taxon:4530"	
/clone="C12645_1A"	
/clone_lib="rice callus cdna"	
/tissue_type="callus"	
/dev_stage="callus"	
BASE COUNT 93 a 155 c 134 g 118 t 4 others	
ORIGIN	

Query Match
Best Local Similarity 52.1% Pred. No. 4.1;
Matches 100; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

OY	3237	caacgcgcaaaagccttgagcgcctgatgttcgagccgcggcgccgatgccttcgagaagacaga	3296
Db	246	CAGCGAGGAGGCGCGTGCAGAACCGTGTTGGAGTGAGGCTGCTCGCGCAGCAGACAGAGG	187
OY	3297	aagcgttcgcaaacgcggccgcggcacggcgaggcgaggaaaatgtcggcatattgacggcgga	3356
Db	186	AGCTGTCCGCCACGCGCGACACCGGATGGGACGCCCTGTGTTGGCGTGGAGAGGGCGGC	127
OY	3357	ggaagagaaaaaaacgggttcgacgcgagtalaagacaacccgttcggcgaacacgcgcgaagc	3416
Db	126	AGGAGAGAGATGTGGCGGAGGAGGWTGGGGCGGACGCCGCCACACCGAGAGACGACGCG	67
OY	3417	ggaaacccgcgcgc 3428	
Db	66	GGAGCACCGGACC 55	

RESULT 28
AG131119
LOCUS AG131119 936 bp DNA linear GSS 04-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-143B12.F., genomic survey sequence.
ACCESSION AG131119

[illegible]

ORGANISM	TITLE
Tetraodon nigroviridis	
Echinozoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Actinopterygii; Neopterygii; Teleostei; Euteleostei;	
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;	
Tetraodontidae; Tetraodon.	
REFERENCE	
1 (bases 1 to 1038)	
Roest-Crolius,H., Jalllon,O., Dasilva,C., Fizesme,C., Fisher,C.,	
Bernot,A., Fizesme,C., Winckler,P., Brottier,P., Quetlier,F.,	
Saurin,W. and Weissenbach,J.	
Bonneau,L., Billault,A., Quetlier,F., Saurin,W., Bernot,A. and	
Weissenbach,J.	
CHARACTERIZATION AND REPEAT ANALYSIS OF THE COMPACT GENOME OF THE	
FRESHWATER PUFFERFISH TETRAODON NIGROVIRIDIS	
JOURNAL	
2 (bases 1 to 1038)	
Roest-Crolius,H., Jalllon,O., Dasilva,C., Bonneau,L., Fisher,C.,	
Bernot,A., Fizesme,C., Winckler,P., Brottier,P., Quetlier,F.,	
Saurin,W. and Weissenbach,J.	
HUMAN GENE NUMBER ESTIMATE PROVIDED BY GENOME WIDE ANALYSIS USING	
TETRAODON NIGROVIRIDIS DNA SEQUENCE	
REFERENCE	
3 (bases 1 to 1038)	
Genoscope.	
JOURNAL	
DIRECT SUBMISSION	
SUBMITTED (12-APR-2000) TO THE EMBL/GENBANK/DBJ DATABASES	
THIS SEQUENCE IS A SINGLE READ AND WAS GENERATED AS PART OF A LARGE	
SCALE CLONE-END SEQUENCING PROJECT OF THE TETRAODON NIGROVIRIDIS	
GENOME. FOR MORE INFORMATION, PLEASE TAKE A LOOK AT	
HTTP://WWW.GENOSCOPE.CNS.FR/TETRAODON.	
LOCATION/QUALIFIER	
1..1038	
/organism="Tetraodon nigroviridis"	
/db_xref="taxon:99883"	
/clone="180310"	
/clone_1lb="c"	
/note="Genoscope sequence ID : COAG180BD05.PI-end : T7"	
BASE COUNT	
341 a 300 c 206 g 187 t 4 others	
ORIGIN	
Query Match 1.0%; Score 45.4; DB 12; Length 1038;	
Best Local Similarity 46.2%; Pred. No. 5.8;	
Matches 151; Conservative 0; Mismatches 176; Indels 0; Gaps 0;	
OY 3612 cgaagaccgcgcgaacgccgttggacaagcgcatccggagaccaccaactacgcttc 3671	
Db 145 CAACAACAGCTGCACGCCACATCTAGTCAGACAAACGCTGCAGCACTCAACAGCCGGTC 204	
OY 3672 gcaagaattccgcgcttacccgcaaacaccgacacctgcccgaatcgytatgcagaanaa 3731	
Db 205 AAACAGCAACTCTGGCAGCAACCACTCCAGAAGAACAAACAGCTGCACCATCTGGTGAGA 264	
OY 3732 cctcgagcagcgcgcgctgcgatcctgttttcgacaaacccgagaccggaanaoccttga 3791	
Db 265 CAAACAGCTGCACCAACGACAAACAGCGCGGCAAAACAGCAACTCACACCAACAAACCCTAG 324	
OY 3792 cgacggcatcggaactcggaacgagccttgccacagcgcgcttttcgaggcataagcgc 3851	
Db 325 AGACAACAGCTGCAGCTACATCTGTGTCGACAAACAGCTGCAGCAACTCAACAGCCGGTC 384	
OY 3852 cgacaggttcacatcgcatcacgacgagcgcgcggttttagcagcggcgagccttcaga 3911	
Db 385 AAACAGCAACTTAGCAGCAACAAACCCGAGAACAAACAGCTGCACCATCTAGTGAGA 444	
OY 3912 cggcaltcggaggaataatccgcgcgcg 3938	
Db 445 CAACAGCTGCAGCAACTACACAGCGC 471	
RESULT 30	
CNS015XR/	
LOCUS	
DEFINITION	
CNS015XR Drosophila melanogaster genome survey sequence T7 end of BAC BACN15017 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.	

FEATURES	source	location/Qualifiers
	1. 1159	/organism="Drosophila melanogaster"
		/plasmid="peloBAC11"
		/db_xref="taxon:7227"
		/clone_11b="DrosBAC"
		/clone="BACN15017"
		/note="end : T7"
BASE COUNT	448 a	36 c 7 g 178 t 490 others
ORIGIN		

[illegible]

RESULT	31
BI2052/c	
LOCUS	
DEFINITION	1211 bp
	DNA
	linear
	GSS 14-MAY-1997
	FI7020-S96 IGF Arabidopsis thaliana genomic clone FI7020, DNA
	sequence.
BI2052	
ACCESSION	
VERSION	GI:2093334
KEYWORDS	GSS.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana

FEATURES	source
Location/Qualifiers	1. 1211
/organism="Arabidopsis thaliana"	
/strain="Columbia"	
/db_xref="taxon:3702"	
/clone="F17020"	
/clone_1lb="IGF"	
/sex="hermaphrodite"	
/note="vector: BelosBAC11; Site_1: EcoRI; Site_2: EcoRI"	
Produced by Thomas Altmann"	
BASE COUNT	361 a 328 c 189 g 330 t 3 others
ORIGIN	

OY	511	gcgaacccgttgtaatgaccagttcatatgatggcggaatatatactgatacaaaat	570
Db	543	GAGGCCAAGATTGTGTTTGGTCATGGGAACCTGGACTATATCTCAATGGAAAT	486
OY	571	taacctgaaccglttcgattcgttggcgaggccaatattggcgtcgtctaagaatg	630
Db	483	GATGGTTTTGGTGTTATGGCTTCCACACAGATATGATTTGAAGATTATATAGAG	422
OY	631	cccataaccgcgaagtccatcatcatattgccagtgcgtatcttgcgtctgtgtgc	690
Db	423	ACAACAGCTGTATGGCGTTTCATTTCACTTTTGAAGTGGCTGTGCACATTGTCCTTC	364
OY	691	aataccttgcacaataatgtagtgcgtgcgtgcacagttcaact	733
Db	363	TGTTCTTTGCTCAAGCTTATCTGAGGATGCAAGAAGACT	321

RESULT	32
BI948506	
LOCUS	937 bp mRNA linear EST 19-OCT-2001
DEFINITION	HVSMEI0009007f Hordeum vulgare spike EST library HVCNDA0012 (Pusarium infected) Hordeum vulgare cDNA clone HVSMEI0009007f, mRNA sequence.
ACCESSION	BI948506
VERSION	EST.
KEYWORDS	GI:16288973
SOURCE	barley,
ORGANISM	Hordeum vulgare
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae ; Triticeae; Hordeum.
REFERENCE	1 (bases 1 to 937)
AUTHORS	Wing, R., Muehlbauer, G.J., Close, T.J., Kleinholz, A., Wise, R., Heinen, S.S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T.,

REFERENCE	1 (bases 1 to 1101)
AUTHORS	Genoscope, Direct Submission
TITLE	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
JOURNAL	Bp 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
COMMENT	- Web : www.genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelBAC11.
FEATURES	Location/Qualifiers
source	1. 1101 /organism="Drosophila melanogaster" /plasmid="pBelBAC11" /db_xref="taxon:7227" /clone_11b="DrosBAC" /clone="BACN16J15" /note="end : SP6"
BASE COUNT	212 a 129 c 108 g 231 t 421 others
ORIGIN	
Query Match	1.0% ; Score 45 ; DB 12 ; Length 1101 ;
Best Local Similarity	17.0% ; Pred. No. 7.5 ; Mismatches 136 ; Indels 0 ; Gaps 0 ;
Matches	58 ; Conservative 145 ;
OY 2938	taccgcagcagacaattgaagctgcgagaaatctcgagagcaactacacttgcgcgtc 2997
Db 1093	TACACATRTSSMWWSYVSVASMAVTVARSAVTSASSVSRRARSAGVSVASAGVRSS 1034
OY 2998	aacaaataccgcgcaagaaccccgcaagctctgcaacaattgacggtgtgtggaagaaagac 3057
Db 1033	GVASASASASTSTGSSSMSSSSSVASAGSSSSSVSSAVASTSTYCSAGVSVRGSVAAK 974
OY 3058	aacaacacgcctgctcggaanaactattaccaccctcgcaaaagcaacacgctgatalgcggc 3117
Db 973	HRSASASNSAVSASMRVAAGASASAGSNVGAAGARSRASARARVASRGRGCGGWSRS 914
OY 3118	gcgtgtgcgttaccacaactatctcgcaagaagcggcgagcttcgcgtgcataatccgtcaaa 3177
Db 913	ASASASSSSAVRMRYSVASASVAAASSSSVASASVSSAGVGVVVASAGSASSA 854
OY 3178	gaacaagagccttcgcgaanaactcgcgcaagcgagagccaaacaaacagcggaataaagac 3237
Db 853	SSVAAAATTAIVSVSVASAAANWSSVASAMTAAATAAANAANVAMCVCRCNSMMWMSCC 794
OY 3238	aagcgcaaaagccttgacgcgtgtattcgcgcgcgcgca 3278
Db 793	CVCASASMCGCCVCSCGAGCCMAMRRGRGRCRGVAGR 753
RESULT 36	
AUI63586	
LOCUS	AUI63586 440 bp mRNA linear EST 14-NOV-2000
DEFINITION	AUI63586 Rice panicle at flowering stage Oryza sativa cDNA clone
ACCESSION	E3242, mRNA sequence.
VERSION	AUI63586
KEYWORDS	AUI63586.1 GI:11171024
SOURCE	EST.
ORGANISM	Oryza sativa.
ORYZA sativa	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
Eriartoideae; Oryzaceae; Oryza.	
1 (bases 1 to 440)	
Sasaki,T. and Yamamoto,K.	
Rice cDNA from panicle at flowering stage (2000)	
Unpublished (2000)	
Contact: Takuji Sasaki	

